

K. d. w. l.  
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## RAW SEQUENCE LISTING

DATE: 04/09/2002

PATENT APPLICATION: US/09/582,397A

TIME: 12:30:07

Input Set : A:\49862seq.txt

Output Set: N:\CRF3\04092002\I582397A.raw

4 <110> APPLICANT: Shizuo AKIRA  
5 Takahiro SHIMADA  
7 <120> TITLE OF INVENTION: IDENTIFICATION OF NOVEL SUBSTRATE I-TRAF  
8 OF IKK-i KINASE  
10 <130> FILE REFERENCE: 49862 (71526)  
12 <140> CURRENT APPLICATION NUMBER: 09/582,397A  
13 <141> CURRENT FILING DATE: 2000-06-24  
15 <160> NUMBER OF SEQ ID NOS: 4  
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 2154  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Human  
24 <400> SEQUENCE: 1

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27	tcaacactac	cagctacctg	cggccccgcg	aggtgcaggt	gagggagttt	gaggtcctgc	180
28	ggaagctgaa	ccaccagaac	atcgtcaagc	tctttgcggt	ggaggagacg	ggcgggaagcc	240
29	ggcagaaggt	actggtgatg	gagtactgct	ccagtgggag	cctgctgagt	gtgctggaga	300
30	gccctgagaa	tgcctttggg	ctgcctgagg	atgagttcct	ggtggtgctg	cgctgtgtgg	360
31	tggccggcat	gaaccacctg	cgggagaacg	gcattgtgca	tcgcgacatc	aagccgggga	420
32	acatcatgcg	cctcgtaggg	gaggaggggc	agagcatcta	caagctgaca	gacttcggcg	480
33	ctgcccggga	gctggatgat	gatgagaagt	tcgtctcggt	ctatgggact	gaggagtacc	540
34	tgcataccga	catgtatgag	cgggcggtgc	ttcgaaagcc	ccagcaaaaa	gcgttcgggg	600
35	tgactgtgga	tctctggagc	attggagtga	ccttgtagca	tgcagccact	ggcagcctgc	660
36	ccttcacccc	ctttggtggg	ccacggcgga	acaaggagat	catgtaccgg	atcaccacag	720
37	agaagccggc	tggggccatt	gcaggtgccc	agaggcgagg	gaacgggccc	ctggagtgga	780
38	gctacaccct	ccccatcacc	tgccagctgt	cactggggct	gcagagccag	ctggtgcccc	840
39	tcctggccaa	catcctggag	gtggagcagg	ccaagtgtct	gggcttcgac	cagttctttg	900
40	cggagaccag	tgacatcctg	cagcgagttg	tcgtccatgt	cttctccctg	tcccaggcag	960
41	tcctgcacca	catctatatc	catgcccaca	acacgatagc	cattttccag	gaggccgtgc	1020
42	acaagcagac	cagtgtggcc	ccccgacacc	aggagtacct	ctttgagggt	cacctctgtg	1080
43	tcctcgagcc	cagcgtctca	gcacagcaca	tcgcccacac	gacggcaagc	agccccctga	1140
44	ccctcttcag	cacagccatc	cctaaggggc	tggccttcag	ggaccctgct	ctggacgtcc	1200
45	ccaagtctgt	ccccaaagtg	gacctgcagg	cggattacaa	cactgccaa	ggcgtgttgg	1260
46	gcgcccggta	ccaggccctg	cggctggcac	gggccctgct	ggatgggcag	gagctaattg	1320
47	ttcgggggct	gcactgggtc	atggaggtgc	tccaggccac	atgcagacgg	actctggaag	1380
48	tggcaaggac	atccctcctc	tacctcagca	gcagcctggg	aactgagagg	ttcagcagcg	1440
49	tggctggaac	gcctgagatc	caggaactga	aggcggctgc	agaactgagg	tccaggctgc	1500
50	ggactctagc	ggaggtcctc	tccagatgct	cccaaaatat	cacggagacc	caggagagcc	1560
51	tgagcagcct	gaaccgggag	ctggtgaaga	gccgggatca	ggtacatgag	gacagaagca	1620
52	tccagcagat	tcagtgtctg	ttggacaaga	tgaacttcat	ctacaaacag	ttcaagaagt	1680
53	ctaggatgag	gccagggctt	ggctacaacg	aggagcagat	tcacaagctg	gataagggtga	1740

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54 atttcagtca tttagccaaa agactcctgc aggtgttcca ggaggagtgc gtgcagaagt 1800
55 atcaagcgtc cttagtcaca cacggcaaga ggatgagggt ggtgcacgag accaggaacc 1860
56 acctgcgcct ggttggtctgt tctgtggctg cctgtaacac agaagcccag ggggtccagg 1920
57 agagtctcag caagctcctg gaagagctat ctcaccagct ccttcaggac cgagcaaagg 1980
58 gggctcaggc ctgcgcgcct cccatagctc cttaccccag ccctacacga aaggacctgc 2040
59 ttctccacat gcaagagctc tgcgagggga tgaagctgct ggcattctgac ctcttgga 2100
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63 <211> LENGTH: 716
64 <212> TYPE: PRT
65 <213> ORGANISM: Human
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70 Gln Gly Ala Thr Ala Ser Val Tyr Lys Ala Arg Asn Lys Lys Ser Gly
71 20 25 30
72 Glu Leu Val Ala Val Lys Val Phe Asn Thr Thr Ser Tyr Leu Arg Pro
73 35 40 45
74 Arg Glu Val Gln Val Arg Glu Phe Glu Val Leu Arg Lys Leu Asn His
75 50 55 60
76 Gln Asn Ile Val Lys Leu Phe Ala Val Glu Glu Thr Gly Gly Ser Arg
77 65 70 75 80
78 Gln Lys Val Leu Val Met Glu Tyr Cys Ser Ser Gly Ser Leu Leu Ser
79 85 90 95
80 Val Leu Glu Ser Pro Glu Asn Ala Phe Gly Leu Pro Glu Asp Glu Phe
81 100 105 110
82 Leu Val Val Leu Arg Cys Val Val Ala Gly Met Asn His Leu Arg Glu
83 115 120 125
84 Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly Asn Ile Met Arg Leu
85 130 135 140
86 Val Gly Glu Glu Gly Gln Ser Ile Tyr Lys Leu Thr Asp Phe Gly Ala
87 145 150 155 160
88 Ala Arg Glu Leu Asp Asp Asp Glu Lys Phe Val Ser Val Tyr Gly Thr
89 165 170 175
90 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
91 180 185 190
92 Pro Gln Gln Lys Ala Phe Gly Val Thr Val Asp Leu Trp Ser Ile Gly
93 195 200 205
94 Val Thr Leu Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Ile Pro Phe
95 210 215 220
96 Gly Gly Pro Arg Arg Asn Lys Glu Ile Met Tyr Arg Ile Thr Thr Glu
97 225 230 235 240
98 Lys Pro Ala Gly Ala Ile Ala Gly Ala Gln Arg Arg Glu Asn Gly Pro
99 245 250 255
100 Leu Glu Trp Ser Tyr Thr Leu Pro Ile Thr Cys Gln Leu Ser Leu Gly
101 260 265 270
102 Leu Gln Ser Gln Leu Val Pro Ile Leu Ala Asn Ile Leu Glu Val Glu
103 275 280 285
104 Gln Ala Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala Glu Thr Ser Asp

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105	290	295	300
106	Ile Leu Gln Arg Val Val Val His Val Phe Ser Leu Ser Gln Ala Val		
107	305	310	315 320
108	Leu His His Ile Tyr Ile His Ala His Asn Thr Ile Ala Ile Phe Gln		
109		325	330 335
110	Glu Ala Val His Lys Gln Thr Ser Val Ala Pro Arg His Gln Glu Tyr		
111		340	345 350
112	Leu Phe Glu Gly His Leu Cys Val Leu Glu Pro Ser Val Ser Ala Gln		
113		355	360 365
114	His Ile Ala His Thr Thr Ala Ser Ser Pro Leu Thr Leu Phe Ser Thr		
115		370	375 380
116	Ala Ile Pro Lys Gly Leu Ala Phe Arg Asp Pro Ala Leu Asp Val Pro		
117	385	390	395 400
118	Lys Phe Val Pro Lys Val Asp Leu Gln Ala Asp Tyr Asn Thr Ala Lys		
119		405	410 415
120	Gly Val Leu Gly Ala Gly Tyr Gln Ala Leu Arg Leu Ala Arg Ala Leu		
121		420	425 430
122	Leu Asp Gly Gln Glu Leu Met Phe Arg Gly Leu His Trp Val Met Glu		
123		435	440 445
124	Val Leu Gln Ala Thr Cys Arg Arg Thr Leu Glu Val Ala Arg Thr Ser		
125		450	455 460
126	Leu Leu Tyr Leu Ser Ser Ser Leu Gly Thr Glu Arg Phe Ser Ser Val		
127	465	470	475 480
128	Ala Gly Thr Pro Glu Ile Gln Glu Leu Lys Ala Ala Ala Glu Leu Arg		
129		485	490 495
130	Ser Arg Leu Arg Thr Leu Ala Glu Val Leu Ser Arg Cys Ser Gln Asn		
131		500	505 510
132	Ile Thr Glu Thr Gln Glu Ser Leu Ser Ser Leu Asn Arg Glu Leu Val		
133		515	520 525
134	Lys Ser Arg Asp Gln Val His Glu Asp Arg Ser Ile Gln Gln Ile Gln		
135		530	535 540
136	Cys Cys Leu Asp Lys Met Asn Phe Ile Tyr Lys Gln Phe Lys Lys Ser		
137	545	550	555 560
138	Arg Met Arg Pro Gly Leu Gly Tyr Asn Glu Glu Gln Ile His Lys Leu		
139		565	570 575
140	Asp Lys Val Asn Phe Ser His Leu Ala Lys Arg Leu Leu Gln Val Phe		
141		580	585 590
142	Gln Glu Glu Cys Val Gln Lys Tyr Gln Ala Ser Leu Val Thr His Gly		
143		595	600 605
144	Lys Arg Met Arg Val Val His Glu Thr Arg Asn His Leu Arg Leu Val		
145		610	615 620
146	Gly Cys Ser Val Ala Ala Cys Asn Thr Glu Ala Gln Gly Val Gln Glu		
147	625	630	635 640
148	Ser Leu Ser Lys Leu Leu Glu Glu Leu Ser His Gln Leu Leu Gln Asp		
149		645	650 655
150	Arg Ala Lys Gly Ala Gln Ala Ser Pro Pro Pro Ile Ala Pro Tyr Pro		
151		660	665 670
152	Ser Pro Thr Arg Lys Asp Leu Leu Leu His Met Gln Glu Leu Cys Glu		
153		675	680 685

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159 <210> SEQ ID NO: 3
160 <211> LENGTH: 2910
161 <212> TYPE: DNA
162 <213> ORGANISM: Mouse
164 <400> SEQUENCE: 3
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167 gaaatccggg gaggtggttg ctgtaaaggc cttcaactca gccagctatc ggcgacctcc      180
168 tgaggttcag gtgagggagt ttgaggtcct gcggaggctg aatcaccaga acatcgtgaa      240
169 gctattcgca gtggaggaaa cgggaggcag ccggcagaag gtgctaatac tggagtactg      300
170 ctccagtggg agcctgctga gcgtgctgga agaccctgag aacacgttcg ggctttctga      360
171 agaggagttc ctagtggctg tgcgctgtgt ggtggctggc atgaaccacc tgcgggagaa      420
172 tggcattgtc categggaca tcaaacctgg gaacatcatg cgcctgggtg gcgaggaggg      480
173 gcagagcadc tataagctgt ctgacttcgg ggctgcccgc aagctggacg atgatgagaa      540
174 gtttgtttct gtctatggta cagaggaata cctgcaccct gacatgtatg agcgtgcagt      600
175 gctgcgcaaa cccagcaaaa aggcatttgg tgtgactgtg gatctctgga gtattggggg      660
176 gacctgttac cagcagccca caggcagtct gcccttcac ccttcgggtg ggccccggcg      720
177 caacaaagag atcatgtaca gaatcaccac agagaagcca gccggggcca ttccagggac      780
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180 ggataagtgc tggggctttg atcagttctt cgcggagacc agtgacattc tgcagcgaac      960
181 ggtcatccac gtcttttccc taccacaggc cgttttgcac catgtctaca tccacgcccc      1020
182 caacacgatt gccatctttt tggaggctgt atatgagcag accaacgtga ccccaaaca      1080
183 ccaggagtac ctcttcgagg gtcacccttg tgtccttgag ccaagcctct cagcccagca      1140
184 catcgcccac acagctgccca gcagccctct aactctgttc agcatgtcca gcgacacacc      1200
185 taaggggctg gccttcaggg accctgctct ggatgtccca aagttcgtcc ctaagggtga      1260
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200 tgatatgaag ctattggcct ttgatctcca ggacaacaac cgactcatcg aacgggtaca      2160
201 tagagtcca tcggcaccag atgtctgagc tccctggggg ttcacaaggc actcagaagc      2220
202 aatagaaaca ttcattattg acccctacac tgtgagacca aattcagggc aagttctggt      2280
203 tccatctcac tagcctacct ccctcttggc cattggccat tggccaacaa actagcatta      2340
204 ctttgactgt cctcttggga agcagctagg acagggactc ctggccatcc caggcagtat      2400

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207 ttcccaggac cagcaggcat ctctgtggc ttctcctgcc tctccagggt gctggatcag 2580
208 aatgcttatt cttcgttggt tcctgtgctg ttctcctgagt gtcccatcc cctggcctca 2640
209 ggcaaccac aaacggcccc tctgtgcttg gtctagatgc acctgcattt gagaaagtgg 2700
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211 cttggttcta agaaacagct ggtcagtatc aaccacagcc atgctaactg gacagatgtt 2820
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216 <211> LENGTH: 717
217 <212> TYPE: PRT
218 <213> ORGANISM: Mouse
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225 Glu Val Val Ala Val Lys Val Phe Asn Ser Ala Ser Tyr Arg Arg Pro
226 35 40 45
227 Pro Glu Val Gln Val Arg Glu Phe Glu Val Leu Arg Arg Leu Asn His
228 50 55 60
229 Gln Asn Ile Val Lys Leu Phe Ala Val Glu Glu Thr Gly Gly Ser Arg
230 65 70 75 80
231 Gln Lys Val Leu Ile Met Glu Tyr Cys Ser Ser Gly Ser Leu Leu Ser
232 85 90 95
233 Val Leu Glu Asp Pro Glu Asn Thr Phe Gly Leu Ser Glu Glu Glu Phe
234 100 105 110
235 Leu Val Val Leu Arg Cys Val Val Ala Gly Met Asn His Leu Arg Glu
236 115 120 125
237 Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly Asn Ile Met Arg Leu
238 130 135 140
239 Val Gly Glu Glu Gly Gln Ser Ile Tyr Lys Leu Ser Asp Phe Gly Ala
240 145 150 155 160
241 Ala Arg Lys Leu Asp Asp Asp Glu Lys Phe Val Ser Val Tyr Gly Thr
242 165 170 175
243 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
244 180 185 190
245 Pro Gln Gln Lys Ala Phe Gly Val Thr Val Asp Leu Trp Ser Ile Gly
246 195 200 205
247 Val Thr Leu Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Ile Pro Phe
248 210 215 220
249 Gly Gly Pro Arg Arg Asn Lys Glu Ile Met Tyr Arg Ile Thr Thr Glu
250 225 230 235 240
251 Lys Pro Ala Gly Ala Ile Ser Gly Thr Gln Lys Gln Glu Asn Gly Pro
252 245 250 255
253 Leu Glu Trp Ser Tyr Ser Leu Pro Ile Thr Cys Arg Leu Ser Met Gly
254 260 265 270
255 Leu Gln Asn Gln Leu Val Pro Ile Leu Ala Asn Ile Leu Glu Val Glu

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VERIFICATION SUMMARY

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